

The Effects of External Pressure and the Genetic Predisposition to Temperamental Behavior

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Abstract

Violent crime can be considered a social epidemic in our society. Although the idea that violence has biological components is not a new one, recent research in genetics has helped to clarify it. However, environmental pressures are essential for an individual to develop violent behavior. In this study, we use a Mendelian model of two alleles at a single locus, where A and a represents low and high predisposition to temperamental behavior. We use a stochastic compartmental model to investigate the dynamics of the population by controlling the environmental and genetic factors and incorporating the effect of interaction with violent people. This study of the dynamics of the population allows us to predict changes in parameters, which in turn may help to decrease violent behavior individuals in the next generations.

1 Background

The Bureau of Justice Statistics and the Federal Bureau of Investigation, as of October 22, 2001, reported that there has been a decline between 1999 and

2000 of serious violent crime levels as measured by the National Crime Victimization survey [2]. Although there has been a decline of 10%, the prison population increased by 45%, and the actual crime incidents are still alarming [3]. In the year 2000, the FBI crime index reported 11,605,751 offenses, in which they included violent crimes of murder, non-negligent manslaughter, forcible rape, robbery, aggravated assault, and property crimes of burglary, larceny-theft, and motor vehicle theft [4]. It has also been reported that one violent crime occurs every 22.1 seconds, one murder every 33.9 minutes and one aggravated assault every 34.6 seconds [5]. This leads to the following question: What are the causes or mechanisms behind violent behavior in the United States population?

Violence is any sorts of behavior that hurts someone or makes them feel afraid, and it is influenced by various factors, both internal and external. There are many different levels of environmental pressures that trigger violent responses by individuals.

Scientists have always suspected that genetics are linked or contribute to violent behavior. Some recent studies have attempted to find a direct correlation between genes and violent behavior. In *An Overview of Biological Influences on Violent Behavior*, it is claimed that even when an individual is exposed to complex social environmental influences, the propensity to engage in violent behavior may eventually be traced to their biologic basis [7] .

2 Introduction

Violent crime is when an offender uses intimidation of physical force resulting in the harm of another person. Examples of violent crime include, but are not limited to: homicide, manslaughter, aggravated assault, and assault causing bodily harm. In this study we define violence as some violent act that you can get punish for, that is, some violent act that implies incarceration. There are factors that may cause violent behavior such as external pressures. We study the effect of these external pressures on individuals with some predisposition to violence and we take into account the environmental pressures and the interaction with violent people as the factors that lead to the manifestation of violent behavior. It is known that the interaction with violent people is also an environmental pressure for the population; however, we separate both of them because we want to know which one has a greater negative influence on the population. Although external pressures induce violent behavior, another

factor that may cause violence is genetics.

Do genetics affect violence? There are studies that have related genetics and violent behavior. In the late 1970s, the American Army scientists discovered the connection between violence and low serotonin (in the brain) while studying servicemen who were habitually violent. Other studies showed how low levels in violent prisoners successfully predicted the ones who were most likely to re-offend on release [8]. These studies confirm that genes affect the production of various chemicals in the body and some relate low serotonin levels with aggressive behavior. The gene coding for this protein maps to chromosomes. Therefore, the genetic variation in the gene coding for this protein could have effects on aggression, a serotonin-related behavior [9].

Due to the alarming statistics on criminality in the United States, we treat violence as an epidemic and we take into account genetic factors and environmental pressures that lead to the manifestation of violent behavior. In fact, our model is geared towards the study of the dynamics of violent behavior in a system that includes genetic and environmental factors. The study of this model may help in the understanding of both the genetic and environmental contributions to the observed variations in human violent behavior. Our increased knowledge on the interplay between genetics and environmental factors may help predict and control violent behaviors in future generations.

In this report we focused on environments that lead some individuals to acts of violence that may result in jail sentences. The probability of going to jail is analytically computed. The expected number of times that an individual goes to jail in his/her life and the amount of time that an individual spends in jail are computed numerically for multiple environments. Also, the long-term dynamics of the population is studied. The report ends with our conclusions and suggestions on how to reduce violence in our society.

3 The Model

3.1 Description of the model

We introduce a stochastic framework that describes the possible outcomes associated with the time evolution of an individual with some genetic predisposition to violence. The flow diagram for this model is shown in Figure 1.

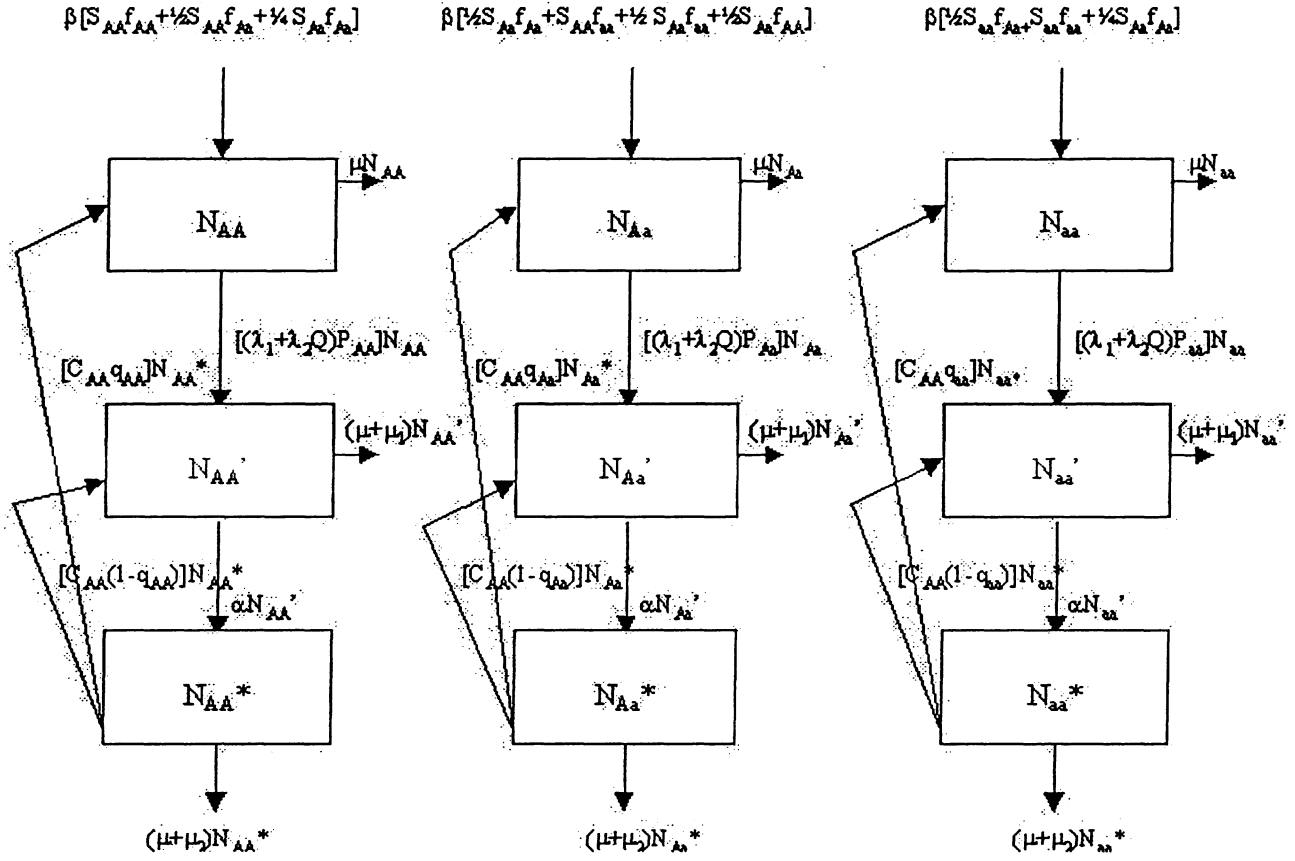


Figure 1: The Transition Diagram

Mendelian genetics are used to classify the genetic predispositions to violence. We assume that genetic predisposition to violent behavior is governed by two alleles at a single locus: allele A (dominant) and allele a (recessive). Three genotypes are then possible: AA (homozygous dominant), Aa (heterozygous) and aa (homozygous recessive). The homozygous genotype aa predisposes violence, and we assume that the heterozygote Aa is somewhat intermediate in terms of the trait that predisposes to violence. The model assumes a constant panmictic population.

Our population is divided in the three behavioral/environmental stages that are shown in Figure 2, where N is the non-violent stage, N' is the violent behavior stage, and N^* the removed (jail) stage for each genotype. An individual is born into the non-violent stage and then moves to the vio-

N	AA	Aa	aa
N'	AA	Aa	aa
N^*	AA	Aa	aa

Figure 2: Behavioral stages

lent behavior stage at a rate determined by the environmental pressure and the genetic mediated peer-pressure. The environmental pressure and the genetic mediated pressure that individuals are putting on the non-violent population remains the same for each of the groups. On the other hand, P_i , the probability that a non-violent individual reacts violently, changes for each group as determined by their genetic predisposition. We assume that $P_{AA} < P_{Aa} < P_{aa}$. Individuals may die in the non-violent stage due to natural causes at a rate of μ ; in the violent stage the death rate is $\mu + \mu_1$, where μ_1 is death related to criminal acts; and, in the removed stage, the death rate is $\mu + \mu_2$, where μ_2 is death in jail not pertaining to natural causes. The death rate for the violent stage is likely to be greater than any of the other death rates since those individuals are more exposed to violence, thus it is assumed that $\mu + \mu_1 > \mu + \mu_2 > \mu$. Once an individual is considered a violent person, then the only way that he/she could rehabilitate is in jail, and they move there at the rate α . Note that α remains the same for the three groups because we assume they are all arrested at the same rate regardless of their genetic predisposition to violence. In jail, a person can either reincorporate into the non-violent stage or the individual can continue to be a delinquent. The rate at which an individual is released from jail (C_{AA} , C_{Aa} ,

C_{aa}), changes for each group because it is assumed that treatment in jail is more effective on homozygous dominant than on the homozygous recessive, that is, $C_{AA} > C_{Aa} > C_{aa}$. Since the homozygous dominant type is more likely to rehabilitate due to its genetic predisposition then the rate at which they incorporate into the non-violent stage is therefore assumed to be greater than the rates of other groups, thus $q_{AA} > q_{Aa} > q_{aa}$.

We use this model to study the expression of the genetic predisposition to violence on the probabilities that individuals act violently (due to social pressures) and on the number of these criminals that actually go to jail. We also want to determine the probability that these individuals are rehabilitated. We also compare these probabilities taking into consideration that we are in charge of controlling parameters that represent external pressures in order to predict the genetic composition of future generations and also the long-term behavior of the system.

3.2 Equations of the model

In this section we study the dynamics of the population for the different genetic predispositions. $N_{AA}(t)$ denotes the number of homozygous dominant individuals at time t ; $N_{Aa}(t)$ the number of heterozygous individuals at time t ; and $N_{aa}(t)$ the number of homozygous recessive individuals at time t . Hence total population of individuals who do not act violently is

$$N = N_{AA} + N_{Aa} + N_{aa}.$$

While the total number of individuals who are expressing violent behavior is

$$N' = N_{AA'} + N_{Aa'} + N_{aa'}.$$

Finally, the population of removed individuals (typically in jail) is

$$N^* = N_{AA^*} + N_{Aa^*} + N_{aa^*}$$

Consequently, the population of free individuals per genotype is

$$\begin{aligned} S_{AA} &= N_{AA} + N_{AA'} \\ S_{Aa} &= N_{Aa} + N_{Aa'} \\ S_{aa} &= N_{aa} + N_{aa'} \end{aligned}$$

with

$$S = N + N'$$

Hence, the proportion of violent individuals in the free population:

$$Q = \frac{N'}{S}$$

The frequency of the alleles in the free population is

$$\begin{aligned} f_{AA} &= \frac{S_{AA}}{S}, \\ f_{Aa} &= \frac{S_{Aa}}{S}, \\ f_{aa} &= \frac{S_{aa}}{S}. \end{aligned}$$

Table 1: Parameter List

Parameters	Description
μ	natural mortality rate
μ_1	mortality rate in the violent environment due to criminal acts
μ_2	mortality rate related to jail
λ_1	influences due to environmental pressures
λ_2	influences due to the interaction with people
β	birth rate per interaction
α	rate at which a violent person goes to jail
P_{AA}, P_{Aa}, P_{aa}	individual's genetic probability of becoming violent
C_{AA}, C_{Aa}, C_{aa}	rate at which the individuals leaves jail
q_{AA}, q_{Aa}, q_{aa}	probability that an individual rehabilitates after jail
f_{AA}, f_{Aa}, f_{aa}	frequency of the allele

Using the above definitions, we arrive at the following model:

$$\begin{aligned}\frac{dN_{AA}}{dt} = & \beta \left[S_{AA}f_{AA} + \frac{1}{2}S_{AA}f_{Aa} + \frac{1}{4}S_{Aa}f_{Aa} \right] \\ & + C_{AA}q_{AA}N_{AA*} - \mu N_{AA} - [(\lambda_1 + \lambda_2 Q)P_{AA}]N_{AA}\end{aligned}$$

$$\begin{aligned}\frac{dN_{AA'}}{dt} = & [(\lambda_1 + \lambda_2 Q)P_{AA}]N_{AA} + C_{AA}(1 - q_{AA})N_{AA*} \\ & - (\mu + \mu_1)N_{AA'} - \alpha N_{AA'}\end{aligned}$$

$$\frac{dN_{AA*}}{dt} = \alpha N'_{AA} - (\mu + \mu_2)N_{AA*} - C_{AA}N_{AA*}$$

$$\begin{aligned}\frac{dN_{Aa}}{dt} = & \beta \left[\frac{1}{2}S_{Aa}f_{Aa} + S_{AA}f_{aa} + \frac{1}{2}S_{Aa}f_{aa} + \frac{1}{2}S_{Aa}f_{AA} \right] \\ & + C_{Aa}q_{Aa}N_{Aa*} - \mu N_{Aa} - [(\lambda_1 + \lambda_2 Q)P_{Aa}]N_{Aa}\end{aligned}$$

$$\begin{aligned}\frac{dN_{Aa'}}{dt} = & [(\lambda_1 + \lambda_2 Q)P_{Aa}]N_{Aa} + C_{Aa}(1 - q_{Aa})N_{Aa*} \\ & - (\mu + \mu_1)N_{Aa'} - \alpha N_{Aa'}\end{aligned}$$

$$\frac{dN_{Aa*}}{dt} = \alpha N_{Aa'} - (\mu + \mu_2)N_{Aa*} - C_{Aa}N_{Aa*}$$

$$\begin{aligned}\frac{dN_{aa}}{dt} = & \beta \left[\frac{1}{2}S_{aa}f_{Aa} + S_{aa}f_{aa} + \frac{1}{4}S_{Aa}f_{Aa} \right] \\ & + C_{aa}q_{aa}N_{aa*} - \mu N_{aa} - [(\lambda_1 + \lambda_2 Q)P_{aa}]N_{aa}\end{aligned}$$

$$\begin{aligned}\frac{dN_{aa'}}{dt} = & [(\lambda_1 + \lambda_2 Q)P_{aa}]N_{aa} + C_{aa}(1 - q_{aa})N_{aa*} \\ & - (\mu + \mu_1)N_{aa'} - \alpha N_{aa'}\end{aligned}$$

$$\frac{dN_{aa*}}{dt} = \alpha N_{aa'} - (\mu + \mu_2)N_{aa*} - C_{aa}N_{aa*}$$

The above equations model the flow of all type of individuals in the population.

4 Results

4.1 Probability that an individual goes to jail

The probability that an individual is removed is the product of the probability that a non-violent individual becomes violent and the probability that a violent individual is removed. These probabilities are denoted by R_1 , R_2 , and R_3 , where R_1 is for the homozygous dominant, R_2 is for the heterozygous and R_3 is for the homozygous recessive. Specifically, we have that

$$R_i = \frac{(\lambda_1 + \lambda_2 Q)P_{jk}\alpha}{((\lambda_1 + \lambda_2 Q)P_{jk} + \mu)(\alpha + \mu + \mu_1)},$$

where $jk = AA, Aa, aa$.

Before analyzing the probabilities for each genotype, we establish the following Lemma:

Lemma 4.1. Suppose $f(x) = \frac{ax+b}{cx+d}$ where $a, b, c, d \geq 0$ and $x_2 \geq x_1$, then

$$\frac{f(x_2)}{f(x_1)} \leq \frac{x_2}{x_1}$$

Proof.

$$\begin{aligned} \frac{f(x_2)}{f(x_1)} &= \left(\frac{ax_2 + b}{cx_2 + d} \right) \left(\frac{cx_1 + d}{ax_1 + b} \right) \\ &= \left(\frac{ax_2 + b}{ax_1 + b} \right) \left(\frac{cx_1 + d}{cx_2 + d} \right) \\ &\leq \frac{ax_2 + b}{ax_1 + b}, \end{aligned}$$

since $\frac{x_1}{x_2} \leq 1$. Then $\frac{cx_1+d}{cx_2+d} \leq 1$, and

$$\begin{aligned} \frac{f(x_2)}{f(x_1)} &= \frac{x_2 \left(a + \frac{b}{x_2} \right)}{x_1 \left(a + \frac{b}{x_1} \right)} \\ &\leq \frac{x_2}{x_1}, \end{aligned}$$

since $\frac{\frac{b}{x_2}}{\frac{b}{x_1}} \leq 1$, then $\frac{a + \frac{b}{x_2}}{a + \frac{b}{x_1}} \leq 1$.

□

Consequences of Lemma 4.1:

Let $f(x) = \frac{(\lambda_1 + \lambda_2 Q)x\alpha}{(\lambda_1 + \lambda_2 Q)\tau x + \mu\tau}$, where $\tau = \alpha + \mu + \mu_1$, then by Lemma 4.1,

$$\frac{f(P_{Aa})}{f(P_{AA})} \leq \frac{P_{Aa}}{P_{AA}}.$$

We conclude that since $f(P_{Aa}) = R_2$ and $f(P_{AA}) = R_1$, then $\frac{R_2}{R_1} \leq \frac{P_{Aa}}{P_{AA}}$.

Similarly,

$$\frac{R_3}{R_2} \leq \frac{P_{aa}}{P_{Aa}}$$

and

$$\frac{R_3}{R_1} \leq \frac{P_{aa}}{P_{AA}}.$$

This implies that the probability that an individual of genotype aa (P_{aa}) is removed (goes to jail) is greater than the probability that an individual of genotype Aa , and AA , respectively. The factor in which the probabilities increase is bounded by the factor $\frac{P_{aa}}{P_{Aa}}$ and $\frac{P_{aa}}{P_{AA}}$, respectively. A similar result is obtained when we compare the probability that an individual of genotype Aa goes to jail, with that of an individual of genotype AA . We conclude that the probability increases and is bounded by the factor $\frac{P_{Aa}}{P_{AA}}$.
 Here,

$$f(x) = \frac{(\lambda_1 P_{AA}\alpha) + \lambda_2 P_{jk}\alpha x}{(\lambda_2 P_{jk}\tau x) + (\lambda_1 P_{jk} + \mu)\tau},$$

where $x = Q$, $\tau = (\alpha + \mu + \mu_1)$ and $jk = AA, Aa, aa$.

By Lemma 4.1, we have

$$\frac{f(Q_2)}{f(Q_1)} \leq \frac{Q_2}{Q_1}. \quad (1)$$

We claim that the function in Equation 1 is increasing:

Let

$$f(x) = \frac{a + bx}{c + dx},$$

where $a = \lambda_1 P_{AA}\alpha$, $b = \lambda_2 P_{jk}\alpha$, $c = (\lambda_1 P_{jk} + \mu)(\alpha + \mu + \mu_1)$, and $d = (\lambda_2 P_{jk})(\alpha + \mu + \mu_1)$.

Now,

$$f'(x) = \frac{bc - da}{(c + dx)^2}.$$

We evaluate the numerator to show that it is increasing because we know that the denominator is always positive:

$$\begin{aligned} & (\lambda_2 P_{jk}^2 \alpha \lambda_1 + \lambda_2 P_{jk} \alpha \mu)(\alpha + \mu + \mu_1) - (\lambda_2 P_{jk}^2 \lambda_2 \alpha)(\alpha + \mu + \mu_1) \\ &= (\lambda_2 P_{jk} \alpha \mu)(\alpha + \mu + \mu_1) > 0. \end{aligned}$$

Considering the proportion of violent individuals with respect to the entire removed population, we conclude that as this proportion increases, the probability that a non-violent individual of any genotype that is removed also increases (annually).

Letting

$$f(x) = \frac{x P_{jk} \alpha + \lambda_2 Q P_{jk} \alpha}{x P_{jk} \tau + (\lambda_2 Q P_{jk} + \mu) \tau},$$

with $x = \lambda_1$, $\tau = \alpha + \mu + \mu_1$ and $jk = AA, Aa, aa$, and using Lemma 4.1

$$\frac{f(x_{1_2})}{f(\lambda_{1_1})} \leq \frac{\lambda_{1_2}}{\lambda_{1_1}}.$$

Consider

$$f(x) = \frac{a + bx}{c + dx},$$

with $a = \lambda_2 Q P_{AA} \alpha$, $b = P_{jk} \alpha$, $c = (\lambda_2 Q P_{jk} + \mu) \tau$, and $d = P_{jk} \tau$.

Now,

$$f'(x) = \frac{bc - da}{(c + dx)^2}.$$

Since the denominator is always positive, we are going to evaluate the numerator to show that it is increasing:

$$(P_{jk} \alpha)(\lambda_2 Q P_{jk} + \mu)(\alpha + \mu + \mu_1) - P_{jk}(\alpha + \mu + \mu_1)(\lambda_2 Q P_{jk} \alpha)$$

$$\begin{aligned}
&= (\lambda_2 \alpha Q P_{jk}^2 + P_{jk} \alpha \mu)(\alpha + \mu + \mu_1) - (\lambda_2 Q P_{jk}^2 \alpha)(\alpha + \mu + \mu_1) \\
&= \mu(\alpha + \mu + \mu_1) > 0.
\end{aligned}$$

Since $f'(x)$ is positive, then $f(x)$ is also increasing.

Analyzing the effects of the environmental pressures on the non-violent individuals, we conclude that as the environmental pressures increase, the probability that a non-violent individual of any genotype goes to jail also increases. Now, by Lemma 3.1 we know that the increment of the probability has to be less than or equal to the increment of the proportion of the environmental pressures.

Let

$$f(x) = \frac{x P_{jk} \alpha + x Q P_{jk} \alpha}{(\lambda_1 P_{jk} + \mu) \tau + x Q P_{jk} \tau},$$

where $x = \lambda_2$, $\tau = \alpha + \mu + \mu_1$ and $jk = AA, Aa, aa$.

By Lemma 4.1,

$$\frac{f(x_{22})}{f(\lambda_{21})} \leq \frac{\lambda_{22}}{\lambda_{21}}.$$

Let

$$f(x) = \frac{a + bx}{c + dx},$$

where $a = \lambda_1 P_{AA} \alpha$, $b = Q P_{jk} \alpha$, $c = (\lambda_1 P_{jk} + \mu) \tau$, and $d = Q P_{jk} \tau$.

Now,

$$f'(x) = \frac{bc - da}{(c + dx)^2}.$$

Since the denominator is always positive, we are going to evaluate the numerator to show that it is increasing:

$$\begin{aligned}
&(Q P_{jk} \alpha)(\lambda_1 P_{jk} + \mu)(\alpha + \mu + \mu_1) - Q P_{jk}(\alpha + \mu + \mu_1)(\lambda_1 P_{jk} \alpha) \\
&= (Q P_{jk}^2 \alpha \lambda_1 + Q P_{jk} \alpha \mu)(\alpha + \mu + \mu_1) - (Q P_{jk}^2 \alpha \lambda_1)(\alpha + \mu + \mu_1) \\
&= Q P_{jk} \alpha \mu(\alpha + \mu + \mu_1) > 0.
\end{aligned}$$

Since the derivative of $f(x)$ is positive, then $f(x)$ is also increasing.

These results are consistent, because the amount of persuasion that a non-violent individual receives in order to commit a violent act also affects the probability that an individual is removed. Thus, as the proportion of persuasions increases, so does the probability that a non-violent individual goes to jail. The increment in the probability has to be less than or equal to the increment in the proportion of persuasion.

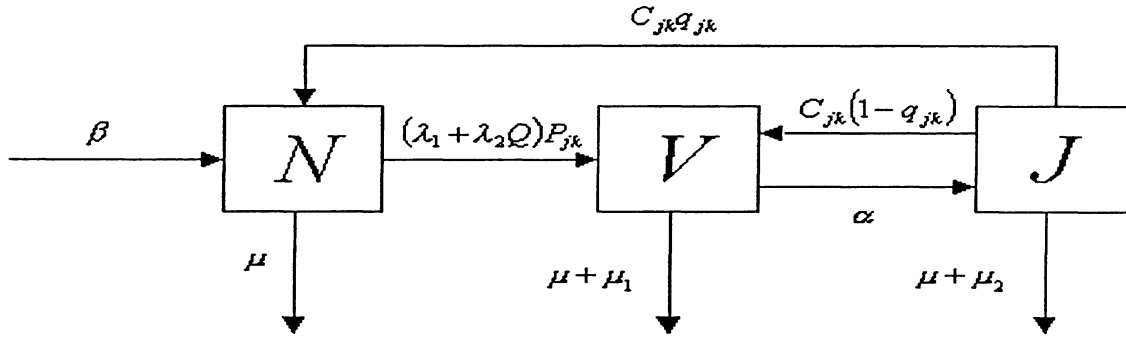


Figure 3: Sub-transition Diagram

4.2 Expected number of times that an individual goes to jail in a lifetime

We use some results about asymptotic behavior of continuous Markov chains discussed in the paper “A Markov Chain Approach to Calculate R_0 in Sto-

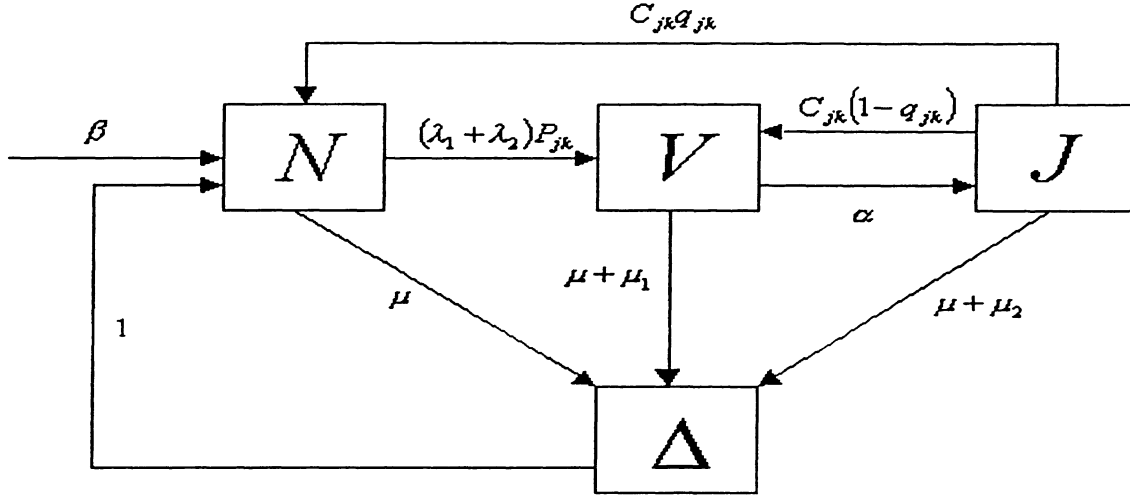


Figure 4: Transition Diagram for a Δ - Cycle

chastic Epidemic Models” by Carlos M. Hernández-Suárez [12]. Consider the flow diagram in Figure 3. Our goal is to calculate the expected number of times that an individual of each genotype goes from state N (Normal-stage) to state J (Jail-stage) in his/her life. The analysis of this problem is equivalent to computing the number of visits to a state r in a Δ - cycle (see Figure 4). A Δ - cycle is the time elapsed between two consecutive returns to the fixed state Δ in the diagram.

Consider the transition rates δ_{ij} of moving from state i to j , where $i \neq j$, and let k_{ij} be the transition probabilities. Let P be the transition matrix of the Markov chain process $\{X_n\}$, where X_n is the state of the process $X(t)$ just after the n^{th} transition. Let τ_r be the first time at which the process makes a transition into state r . The expected number of visits to state r in

a Δ - cycle is given by

$$E[N_r] = \frac{\Pi_r}{\Pi_\Delta},$$

where Π_r is the element corresponding to the state r in the process that takes place in a finite time.

The stationary distribution vector $\Pi = \{\Pi_1, \Pi_2, \Pi_3, \dots, \Pi_\Delta\}$ satisfies the property of a long-term equilibrium, $\Pi = \Pi P$, and can be found by $\Pi = 1(P + J - I)^{-1}$, where P is the matrix of transition probabilities, 1 is a row vector of ones, J is a matrix of ones, and I is the identity matrix.

Applying this process we are able to find the expected number of times that an individual of each genotype is removed (jail) in his/her lifetime, namely

$$\begin{aligned} NT_{AA} &= (C_{AA} + \mu + \mu_2)P_{AA}\alpha(\lambda_1 + \lambda_2 Q) / \\ &\quad (P_{AA}(\lambda_1 + \lambda_2 Q)[(C_{AA}(\mu + \mu_1) + (\mu + \mu_1 + \alpha)(\mu + \mu_2))] \\ &\quad + \mu[C_{AA}(q_{AA}\alpha + \mu_1 + \mu) + (\alpha + \mu + \mu_1)(\mu + \mu_2)]) \\ NT_{Aa} &= (C_{Aa} + \mu + \mu_2)P_{Aa}\alpha(\lambda_1 + \lambda_2 Q) / \\ &\quad (P_{Aa}(\lambda_1 + \lambda_2 Q)[(C_{Aa}(\mu + \mu_1) + (\mu + \mu_1 + \alpha)(\mu + \mu_2))] \\ &\quad + \mu[C_{Aa}(q_{Aa}\alpha + \mu_1 + \mu) + (\alpha + \mu + \mu_1)(\mu + \mu_2)]) \\ NT_{aa} &= (C_{aa} + \mu + \mu_2)P_{aa}\alpha(\lambda_1 + \lambda_2 Q) / \\ &\quad (P_{aa}(\lambda_1 + \lambda_2 Q)[(C_{aa}(\mu + \mu_1) + (\mu + \mu_1 + \alpha)(\mu + \mu_2))] \\ &\quad + \mu[C_{aa}(q_{aa}\alpha + \mu_1 + \mu) + (\alpha + \mu + \mu_1)(\mu + \mu_2)]) \end{aligned}$$

Analysis

The parameters were set after studying some statistics of the United States and by making some assumptions.

We varied the parameter Q , proportion of violent individuals in the free population, because we wanted to know how the number of violent individuals affect the number of times that an individual is removed given a constant number of environmental pressures and a constant number of interactions. We were also interested in varying λ_1 , environmental pressures, and λ_2 , interactions with people, to see how these pressures affect the number of times

Table 2: Estimated Parameter Values

Parameters	Values	Parameters	Values
μ	$\frac{1}{70}$	α	$\frac{1}{2}$
$\mu 1$	$\frac{2}{70}$	P_{AA}	$\frac{1}{1000}$
$\mu 2$	$\frac{1}{140}$	P_{Aa}	$\frac{1}{800}$
C_{AA}	1	P_{aa}	$\frac{1}{500}$
C_{Aa}	$\frac{1}{3}$	λ_1	12
C_{aa}	$\frac{1}{9}$	λ_2	100
q_{AA}	0.9	Q	$\frac{5}{98,5}$
q_{Aa}	0.3	β	$\frac{2}{70}$
q_{aa}	0.1	$N + N' + N^*$	500,000

that a person is removed and if there is any difference between the environmental and the peer pressure. While we varied the proportion of violent individuals in the free population, environmental pressures and interactions with people we set the other parameters with the values in Table 2.

4.2.1 Changing the proportion of violent individuals in the free population (Q).

The number of times that an individual goes to jail increases in all the genotypes as the proportion of violent individuals in the free population increases (See Appendix A, Figure 8). The number of times that a homozygous dominant (AA) individual goes to jail is less than the other two because those individuals are less genetically predisposed to be violent. However, when the proportion of violent individuals is almost 73% of the free population, the homozygous recessive (aa) individuals go to jail or are removed the same number of times as the homozygous dominants (AA). In addition, the homozygous dominant (AA) individuals go less because these individuals spend more time in jail. At the initial dynamic the individuals that are more predisposed to be violent go to jail or are removed more times, but when 14 percent of the free individuals are violent they go the same number of times as the heterozygous (Aa) individuals. After some generations, they go less number of times. The number of times in jail or are removed of a heterozygous individual (Aa) grows faster because they depend on the environmental

influences for the expression of violent behavior. In general, we can say that the strongly predisposed individuals go more times to jail when there are few violent individuals in the free population because they do not need a lot of pressures to act violently as the other genotypes. As the proportion of violent individuals in the free community grows the homozygous recessive (aa) or the more predisposed individuals go less number of times to jail because they spend more time there.

4.2.2 Changing the rate of environmental pressures (λ_1).

We observe an increase in the number of times that an individual goes to jail or is removed when the environmental pressures λ_1 changes (See Appendix A, Figure 8). In fact, the number of times that an individual goes to jail increases quickly in the first 50 events per year because these are more significant events. It is almost sure that a person is going to react to these numbers of events, and consequently, some individuals act violently. There is a stable number of times that an individual goes to jail, which is the number of times that the individual of that genotype is going to jail after becoming violent. After λ_1 is greater than 230 the homozygous dominant (AA) and the heterozygous individuals (Aa) have the same number of times in jail, but after that the heterozygous (Aa) becomes stabilized. With λ_1 equals to 315 the homozygous dominant (AA) and the homozygous recessive (aa) individuals go to jail the same number of times. The homozygous dominant (AA) needs more environmental pressures to achieve a stable number because they are genetically less predisposed to violent behavior. The opposite happens with the homozygous recessive (aa).

4.2.3 Changing the rate of interactions with other people (λ_2).

The number of times that an individual goes to jail increases as the interactions with other people increase (See Appendix A, Figure 8). The increment in this parameter has more affect on the heterozygous individuals. These have the same number of times in jail or removed than the homozygous recessive after 279 interactions with people, then they go more times. The same happens with the homozygous dominant and recessive after 1437 interactions. We observed that this behavior is the same that we obtained with

the variation of the proportion of violent individuals in the free population, because they are intimately related.

4.3 Expected amount of time that an individual spends removed or in jail

Considering the stationary distribution vector Π described in the previous section, $\Pi = \{\Pi_1, \Pi_2, \Pi_3, \dots, \Pi_\Delta\}$, we can calculate the expected amount of time that an individual spends in jail. The expected time that an individual spends in jail is the product of the expected number of times that an individual goes to jail and the average time spent in jail. Therefore, it is given by the following equation:

$$NT_{jk} \cdot \frac{1}{C_{jk} + \mu + \mu_1},$$

where $jk = AA, Aa, aa$.

Thus, the expected number of times that an individual of each genotype spends in jail, denoted by T_{AA} , T_{Aa} , and T_{aa} , respectively, are given by

$$\begin{aligned} T_{AA} &= NT_{AA} \cdot \frac{1}{C_{AA} + \mu + \mu_2} \\ T_{Aa} &= NT_{Aa} \cdot \frac{1}{C_{Aa} + \mu + \mu_2} \\ T_{aa} &= NT_{aa} \cdot \frac{1}{C_{aa} + \mu + \mu_2} \end{aligned}$$

Numerical Studies

We use the same basic parameters of Subsection 3.2.

4.3.1 Changing the proportion of violent individuals in the free population (Q).

In this graph we observe that as the proportion of violent individuals increases in the free community, the amount of time that a person spends in jail, for

the three genotypes increases (See Appendix A, Figure 9). The homozygous recessive (aa) individuals spend a lot more time in jail than the other two genotypes. And the homozygous dominant (AA) individuals go to jail for a relative shorter time.

4.3.2 Changing the rate of environmental pressures (λ_1).

As the environmental pressures increase the time that an individual spends in jail increases as well (See Appendix A, Figure 9). While λ_1 increases, at the beginning, the time that a person spends in jail increases more quickly because the first traits are more sensitive to changes in behavior. Also, we note that the environmental pressures do not increase significantly the amount of time that those individuals spend in jail. The amount of time that a heterozygous individual (Aa) spends in jail where there is significant environmental pressures is going to be similar to the amount of time spent in jail by a homozygous recessive (aa) individual.

4.3.3 Changing the rate of interactions with other people (λ_2).

The interactions with people (peer-pressure) also increase the amount of time that an individual spends in jail (See Appendix A, Figure 9). All the genotypes increase similarly and the amount of time that one genotype spends in jail is never the same as another genotypes. The amount of time that a homozygous dominant (AA) spends in jail is always less than the amount of time of the heterozygous (Aa). Furthermore, the amount of time in jail for the heterozygous (Aa) is always less than the amount of time for the homozygous recessive (aa).

5 Dynamics of the system

The purpose of this section is to study the dynamics in the populations of different genotypes; we also wish to study the impact of varying some parameters on the dynamics of each genotype at any given stage. After running various simulations, we decided to focus our attention on the effects of environmental and peer-pressure from violent individuals because these parameters determine the rate at which an individual moves from the non-violent stage to the violent stage. Once in the violent stage, the only way out is either by going to jail or dying. Thus, placing our attention on the

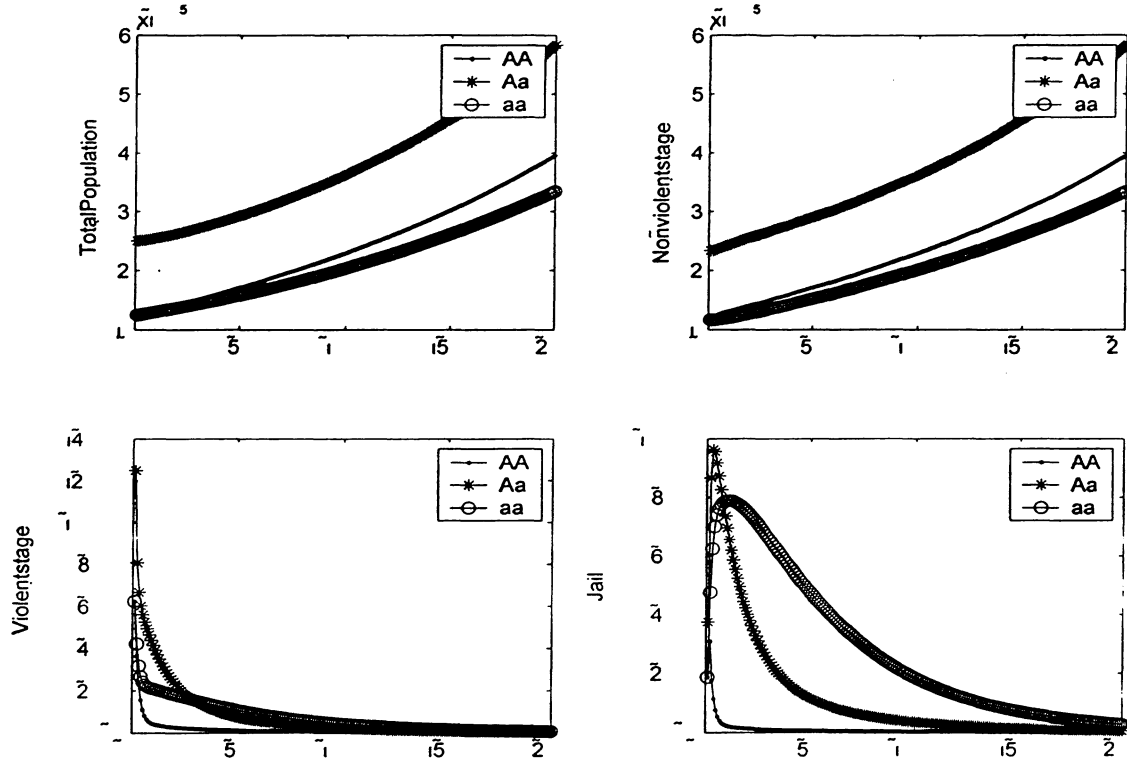


Figure 5: Having no environmental pressures $\lambda_1 = 0$

parameters that trigger the flow of our model will better help us understand the dynamics of the population at any given stage.

5.1 Having no environmental pressures $\lambda_1 = 0$

In this section, we use for illustration purposes the same parameters discussed in the previous section. We let our population size be 500,000, which represents a mid-size city of the United States, and run simulations for a period of 200 years (See Figure 5).

In this simulation we are focusing on the effects of the interaction with other violent individuals, thus we let $\lambda_1 = 0$. When we look at the non-violent population we can see that the population of all three genotypes is surviving and growing, with respect to time. Another interesting thing to notice is that the population of genotype Aa , individuals who are interme-

diately predisposed to violence, is roughly twice the size of the other two genotypes. This behavior maintains frequencies expected under the Hardy-Weinberg equilibrium.

From the graph of the violent stage we observe that the population of all three genotypes decreases and eventually goes to extinction. The population of genotype AA drops at a greater rate, in a shorter amount of time, when compared to the other genotypes. In the long run, less people are going to become violent because most of the population of genotype aa and Aa are in jail. Therefore, the non-violent individuals are moving to the violent stage at a low rate. A different interpretation of this is that the violent individuals are moving to jail at a fast rate and there is no non-violent individuals moving to the violent stage. Eventually, the violent population is going to be small enough that the pressure that they put on the non-violent individuals is not going to be effective and since we are assuming that there is no environmental pressure, then we are going to end up having an ideal situation. In other words, violence decreases and eventually it disappears in the society. The same dynamics is observed in the jail population, where you have individuals of the three genotypes decrease and eventually die out. From this simulation, our model is suggesting that one way to eliminate violence is by eliminating environmental pressures.

5.2 Having no influences due to people interaction

$$\lambda_2 = 0$$

The same parameters are used, and now we let $\lambda_1 = 12$, environmental pressures acts per year. We let our population size to 500,000 and we run simulations for a period of 200 years (See Figure 6).

In the non-violent stage, the population of genotype AA is increasing at a faster rate, while the populations of the other genotypes is decreasing at a lower rate that seems as if it were stable. Furthermore, in the first years there is an increase of violent individuals with genotypes aa , Aa , this is attributed to the genetic predisposition to violence of each genotype. Individuals of genotypes Aa and aa are more prone to react violently than the individuals of the homozygous dominant class. As for the individuals of genotype AA , there is a drop since they are less predisposed to react violently to environmental pressures. The sudden decrease in individuals of genotype AA , in the early years, is replaced with a steady increase, simultaneously as the populations

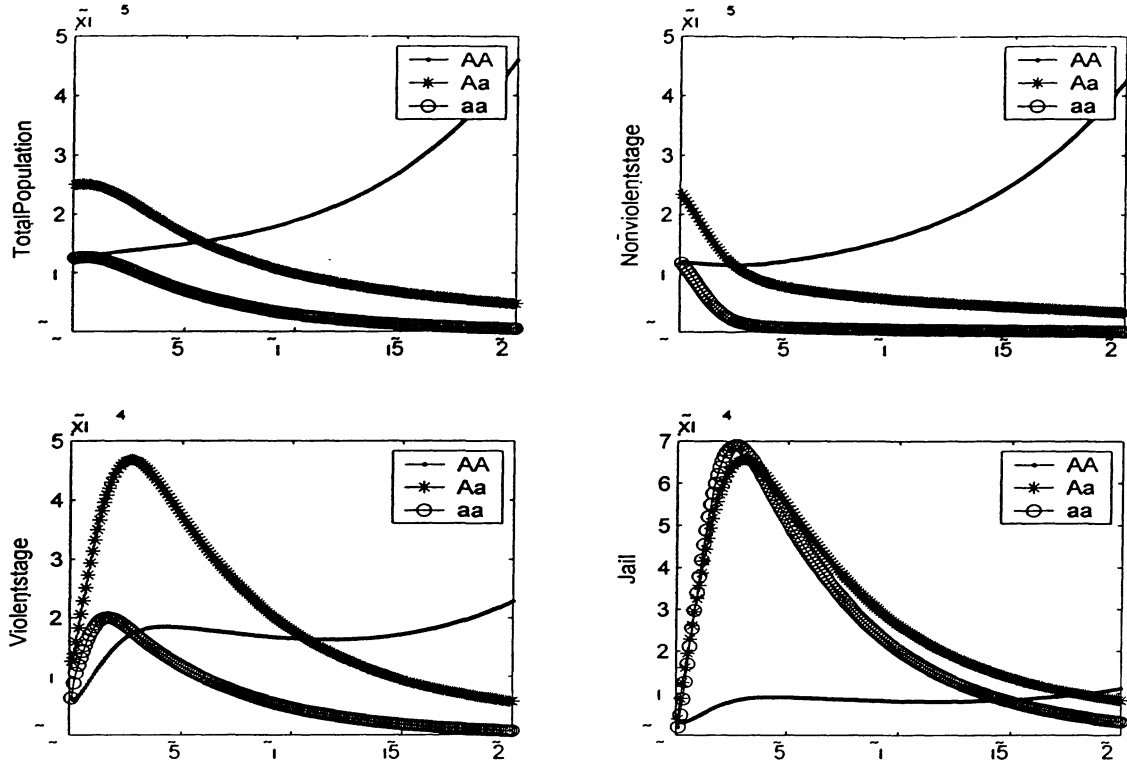


Figure 6: Having no influences due to people interaction $\lambda_2 = 0$

of the other genotypes begins to drop, especially that of genotype aa . The dynamics of the population genotype AA exhibits steady increase, it increases to such a point that the population of the other genotypes go to extinction.

As for the population in jail, both genotypes aa and Aa go to extinction. This is due to the fact that in jail there is no reproduction, thus once an individual of that genotype goes to jail, they spend more time in jail than the individuals of genotype AA . The population of genotype AA in jail increases because, in the long term, the population of the other genotypes is going to become extinct. Thus the only people that will be going to jail are the individuals of genotype AA . When we have no influence due to interactions with violent people, our model is suggesting that we are going to have a less genetically diverse group and although the only genotype that prevails is the one that is not genetically predisposed to violence, violence still exists.

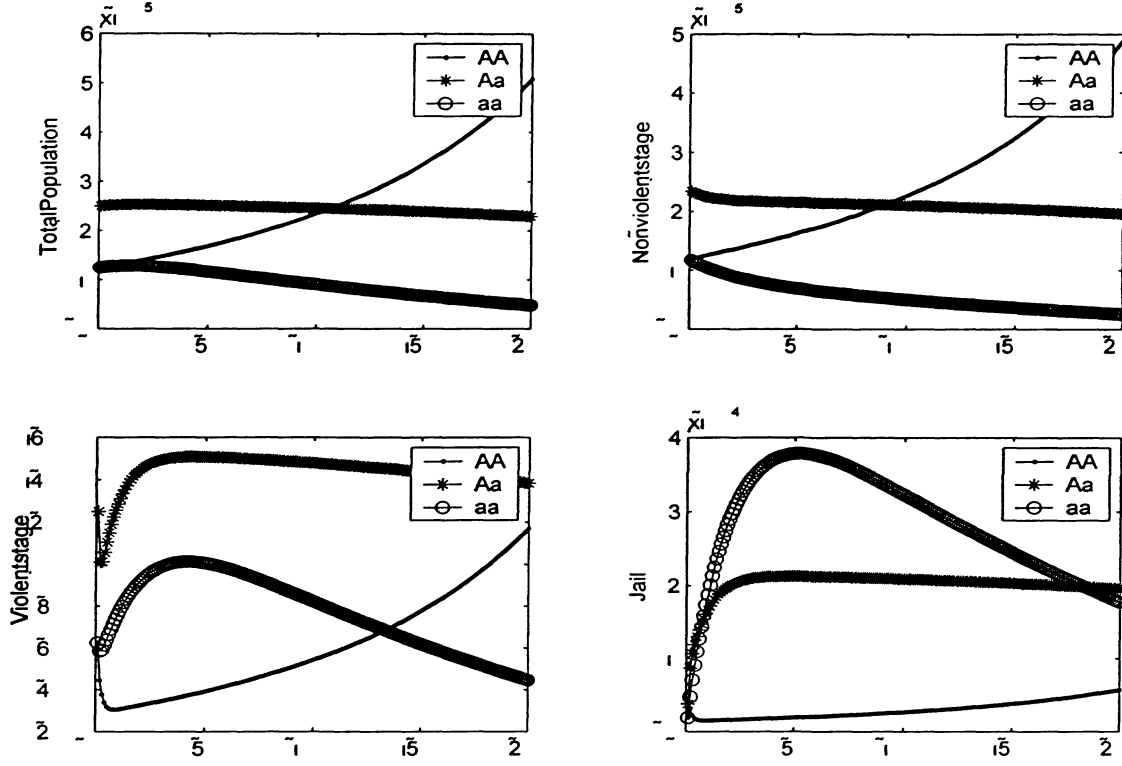


Figure 7: Having the same environmental pressures as influences due to people interaction $\lambda_1 \sim \lambda_2$

5.3 Equivalent environmental and peer-pressures case $\lambda_1 \sim \lambda_2 Q$

In this section, we want to analyze the effects of equivalent external pressures on the population, that is, we consider the case $\lambda_1 \sim \lambda_2 Q$ (See Figure 7). The other parameters stay the same and $\lambda_1 = 12$ and $\lambda_2 = 250$. $\lambda_2 = 250$ because it is being multiplied by the Q , the violent population with respect to the free population, thus $\lambda_2 * Q = 12.7$.

The population of genotype aa , in the non-violent stage decreases in the first years at a fast rate. Simultaneously, the population of this genotype increases in the violent stage but soon begins to decrease and in the long run it becomes extinct, because they are moving to jail at a faster rate than any of the other genotypes. As for the dynamics of this genotype in jail, the population increases steeply but after roughly 60 years, it begins to decrease

at a high rate, until it becomes extinct. The sudden burst of the population of genotype aa in jail is due to the fact that the individuals of this genotype are moving from one compartment to the next at a fast rate, since there is an equal amount of environmental pressure and peer-pressure from violent individuals. Once most people of genotype aa are in jail, then the total population of this genotype goes to extinction, this is due to the fact that in jail there is no reproduction, and since most are in jail, then the genotype is going to disappear.

The dynamics of the population of genotype Aa is as follows. The long-term behavior of this population in the non-violent stage tends to decrease with the years. This decrease is due to the fast rate at which it is moving to the violent stage, thus the population of genotype Aa in the violent stage is on a steady rise for the first 40 years and then there is a steady decrease. This decrease happens because individuals are going to jail at a fast rate. Similarly, in jail there is also a steady increase of population of genotype Aa . Once in jail, and after that steady increase, there is a drastic decrease which is due to the fact that in jail, there is no reproduction and since most of the population of this genotype is in jail then the genotype slowly begins to disappear from the total population, thus the population of genotype Aa decreases in the total population of this genotype.

The population with genotype AA , behaves differently from the other two genotypes. In the non-violent stage, there is a steady rise of the population, which in part is due to low rate in which the individuals are moving to the violent stage. This implies that environmental and peer pressures from other violent individuals, are affecting a small amount of these individuals. Meanwhile, in the violent stage, there is an increase in the first 40 years and after that there is a monotone behavior, for roughly 100 years, which is partly due to the decrease of the other genotypes in the violent population thus there is less pressure coming from the violent individuals, most of the pressure is coming from the environment. Since the population of genotype AA that is in the violent stage is behaving monotone, then it forces the behavior of AA in jail to also be monotone. Since, the population of the other genotypes is going to jail at a higher rate and their sentences are longer than the population of genotype AA , then they are reproducing less. This behavior is unfavorable to the genotype Aa and aa because in the long run the only individuals that are reproducing and surviving are of genotype AA . After analyzing this dynamics, we can conclude that when we have environmental pressures, when λ_1 is positive, then the effects are similar. In

other words λ_1 is driving the dynamics of our population.

6 Conclusions and Future Work

In this research, we analyzed the role that external pressures, such as environmental pressures and influences from violent individuals (peer-pressure), have on individuals who are genetically predisposed to violence. The system was model as a two-allele single locus genetic system and Hardy-Weinberg proportions were initially assumed. We then varied the parameters representing environmental and peer-pressure from violent individual, λ_1 and λ_2 , respectively, and followed the dynamics of the population of each genotype. After running various simulations, fixing all the parameters but varying λ_1 and λ_2 , we conclude that λ_1 , the environmental pressures, has a stronger negative influence on non-violent individuals than interaction with violent people. Also, we saw in our simple Mendelian model that genetics do not have a significant effect in violent behavior in the presence of environmental pressures.

After numerically analyzing the dynamics of our model, we make three suggestions that could help reduce violence. The first one is to reduce environmental pressures. Thus, individuals who are genetically predisposed to violence will become violent at a low rate. We also suggest not focusing on genetics in order to solve violence because the results of our model indicate that in the presence of environmental pressures, genetics do not have a stronger effect on the individuals with some predisposition to violence. The last suggestion, which is an extreme, is to send every violent individual to jail. We suggest this for two reasons: one because they will not have time to place pressure on the non-violent individuals, thus less people will become violent. Second, because once in jail, they cannot reproduce. Putting every violent individual in jail would help reduce violence; doing so is practically impossible because there is not enough jail space for all of the violent individuals, which is a problem that the United States is currently facing. Furthermore, the justice system is not blend and many mistakes and abuses are made. Extending jail sentences for violent offenders is likely to help.

Our approach to this model was primarily simulation based. Thus, for future work, we suggest an analytical approach, were one can discretize the nonlinear system of nine partial difference equations, in order to do some stability analysis and find equilibrium points.

7 Acknowledgements

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References

- [1] *Being Violent* <http://reachout.socialchange.net.au/factsheet/violent-19980224.html>
- [2] *Social Statistics Briefing Room* <http://www.whitehouse.gov/fsbr/crime.html>
- [3] *Neuropsychopharmacology of Pathological Aggression and Sexuality* <http://www.cpa-apc.org/Publications/Archives/CJP/2001/Feb/guest.asp>
- [4] *Crime Index Offenses Reported* <http://www.fbi.gov/ucr/cius-00/00crime2.pdf>
- [5] *Summary of the Uniform Crime Reporting (UCR) Program* <http://www.fbi.gov/ucr/cius-00/00crime1.pdf>
- [6] *Can Genetics Cause Crime?* <http://www.essaymill.com/free-essays/innerns>

- [7] *An Overview of Biological Influences on Violent Behavior*
<http://www.nap.edu/books/0309046491/html/1.html>
- [8] *Reducing violent criminals' serotonin levels*
<http://www.globalideasbank.org/crespec/CS-72.html>.
- [9] *Serotonin Transporter Protein Gene Polymorphism and Personality Measures in African American and European American Subjects*
<http://ajp.psychiatryonline.org>.
- [10] D. L. Hartl, D. Freifelber & L. A. Snyder , *Basic Genetics*, Jones and Bartlett Publishers, 7-27, 1988.
- [11] R. Wachbroit, & D. Wasserman, *Genetics and Criminal Behavior*, Cambridge Press, U.S., 2001.
- [12] Hernández-Suárez, C. M., *A Markov Chain Approach to Calculate R_0 in Stochastic Epidemic Models*, Journal of Theoretical Biology, U.S., 85-86, 2002.

8 Appendix A

```
%function V = violence(howmany)

function V = violence(beta,lambda1,lambda2,alpha,mu,mu1,mu2,P1,P2,P3,
                      CAA,CAa,Caa,q1,q2,q3,N,howmany)

% Initial populations
NAA = (0.935/4)*N;
NAAp = (0.05/4)*N;
NAAs = (0.015/4)*N;
NAa = (0.935/2)*N;
NAap = (0.05/2)*N;
NAas = (0.015/2)*N;
Naa = (0.935/4)*N;
Naap = (0.05/4)*N;
Naas =(0.015/4)*N;

V(1,:) = [1 NAA NAAp NAAs NAa NAAp NAas Naa Naap Naas];
```

```

for gen = 2 : howmany

    % Next generation
    Np = NAAp + NAap + Naap;    % Adding total from second row

    % Total population of free individuals
    S = NAA + NAa + Naa + Np;

    % Proportion of violent individuals with respect to
    % the total population outside jail
    Q = Np/S;

    % Population of free individuals in each genotype
    SAA = NAA + NAAp;
    SAa = NAa + NAap;
    Saa = Naa + Naap;

    % Frequency of the alleles in each genotype for the free population
    fAA = SAA / S;
    fAa = SAa / S;
    faa = Saa / S;

    % The rate of change in each one of the stages
    dNAA = beta*(SAA*fAA + (1/2)*(SAA*fAa) + 1/4*(SAa*fAa)) + (CAA*q1)*NAAs
           - (mu*NAA) - ((lambda1+lambda2*Q)*P1)*NAA;
    dNAAp = ((lambda1+lambda2*Q)*P1)*NAA + CAA*(1-q1)*NAAs - (mu+mu1)*NAAp
            - (alpha*NAAp);
    dNAAs = (alpha*NAAp) - (mu+mu2)*NAAs - (CAA*NAAs);

    dNAa = beta*((1/2)*(SAa*fAa) + SAA*faa + (1/2)*(SAa*faa)
                + (1/2)*(SAa*fAA)) + (CAa*q2)*NAas - (mu*NAa)
            - ((lambda1+lambda2*Q)*P2)*NAa;
    dNAap = ((lambda1+lambda2*Q)*P2)*NAa + CAa*(1-q2)*NAas - (mu+mu1)*NAap
            - (alpha*NAap);
    dNAas = (alpha*NAap) - (mu+mu2)*NAas - (CAa*NAas);

    dNaa = beta*((1/2)*(Saa*fAa) + Saa*faa + 1/4*(SAa*fAa)) + (Caa*q3)*Naas

```

```

        - (mu*Naa) - ((lambda1+lambda2*Q)*P3)*Naa;
dNaap = ((lambda1+lambda2*Q)*P3)*Naa + Caa*(1-q3)*Naas - (mu+mu1)*Naap
        - (alpha*Naap);
dNaas = (alpha*Naap) - (mu+mu2)*Naas - (Caa*Naas);

% Current total population in each stage
NAA = (NAA + dNAA);
NAA = max(NAA, 0);
NAAp = (NAAp + dNAAp);
NAAs = (NAAs + dNAAs);
NAa = (NAa + dNAa);
NAa = max(NAa, 0);
NAap = (NAap + dNAap);
NAas = (NAas + dNAas);
Naa = (Naa + dNaa);
Naa = max(Naa, 0);
Naap = (Naap + dNaap);
Naas = (Naas + dNaas);

V(gen,:) = [gen NAA NAAp NAAs NAa NAap NAas Naa Naap Naas];

V1(gen,:) = [gen dNAA dNAAp dNAAs dNAa dNAap dNAas dNaa dNaap dNaas];

end;

% Total population for each genotype
AA=V(:,2)+V(:,3)+V(:,4);    % total AA
Aa=V(:,5)+V(:,6)+V(:,7);    % total Aa
aa=V(:,8)+V(:,9)+V(:,10);    % total aa
V=[V AA Aa aa];

% Plotting the results
subplot(221),plot(V(:,1),V(:,11),'.-',V(:,1),V(:,12),'*-',V(:,1),V(:,13),'o-')
hold on
xlabel('t (years)')
ylabel('Total Population')
legend('AA', 'Aa', 'aa')
subplot(222),plot(V(:,1),V(:,2),'.-',V(:,1),V(:,5),'*-',V(:,1),V(:,8),'o-')

```

```

xlabel('t (years)')
ylabel('Non-violent stage')
legend('AA', 'Aa', 'aa')
subplot(223),plot(V(:,1),V(:,3),'.-',V(:,1),V(:,6),'*-',V(:,1),V(:,9),'o-')
xlabel('t (years)')
ylabel('Violent stage')
legend('AA', 'Aa', 'aa')
subplot(224),plot(V(:,1),V(:,4),'.-',V(:,1),V(:,7),'*-',V(:,1),V(:,10),'o-')
xlabel('t (years)')
ylabel('Jail')
legend('AA','Aa','aa')
hold off

```

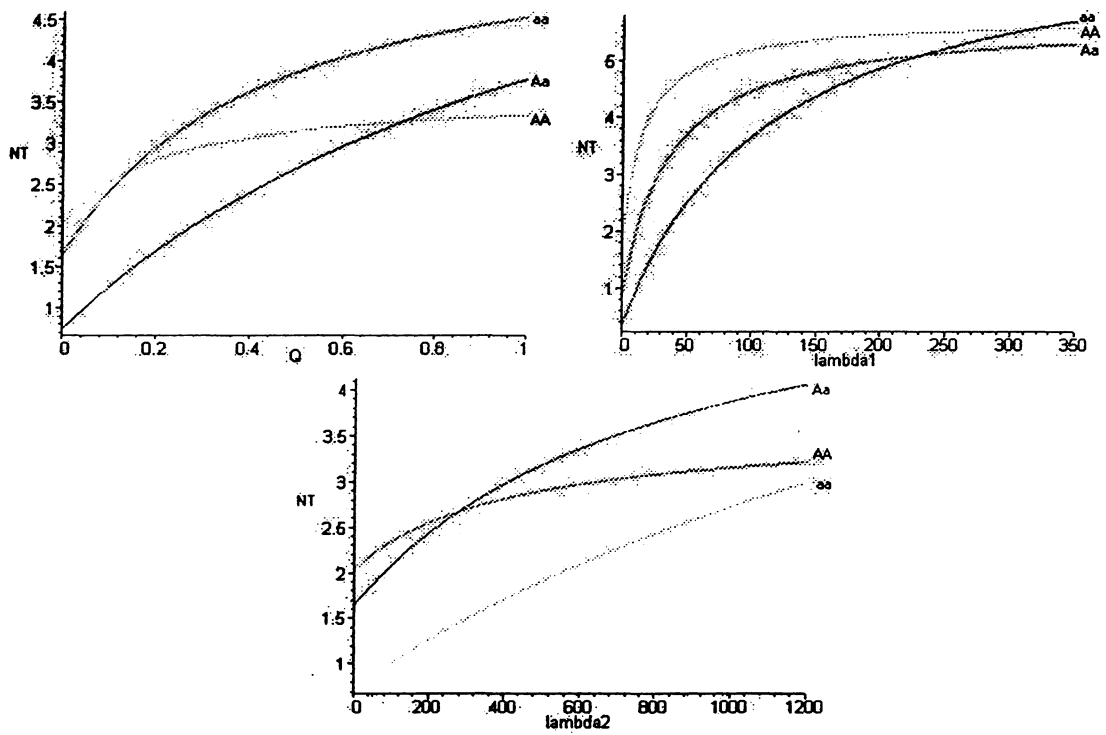


Figure 8: Expected number of times that an individual goes to jail in a life time

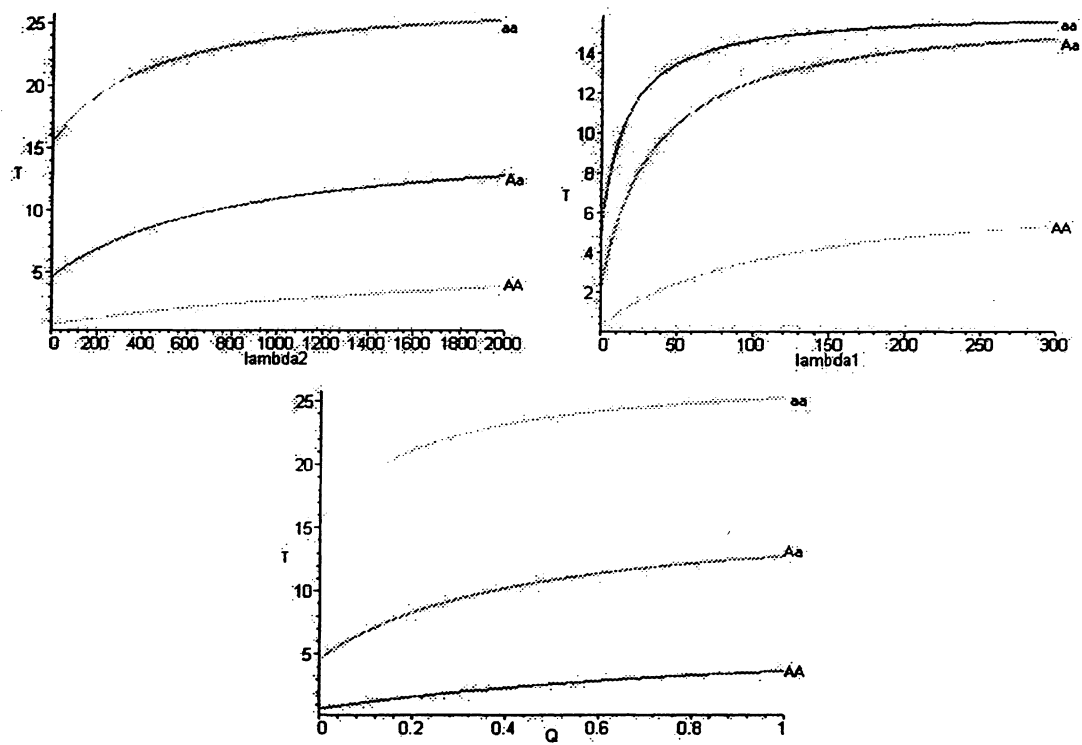


Figure 9: Expected amount of time that an individual spends in jail